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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/086,623

DATE: 03/14/2002 P.S.  
TIME: 12:27:56

Input Set : A:\10086623.txt  
Output Set: N:\CRF3\03142002\J086623.raw

4 <110> APPLICANT: ERIKSSON, Ulf  
5 AASE, Karin  
6 LI, Xuri  
7 PONTEN, Annica  
8 UUTELA, Marko  
9 ALITALO, Kari  
10 OESTMAN, Arne  
11 HELDIN, Carl-Henrik  
13 <120> TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND  
USES THEREOF  
16 <130> FILE REFERENCE: 1064/44833C2  
C--> 19 <140> CURRENT APPLICATION NUMBER: US/10/086,623  
C--> 19 <141> CURRENT FILING DATE: 2000-03-04  
19 <150> PRIOR APPLICATION NUMBER: US 60/107,852  
20 <151> PRIOR FILING DATE: 1998-11-10  
23 <150> PRIOR APPLICATION NUMBER: US 60/113,997  
24 <151> PRIOR FILING DATE: 1998-12-28  
27 <150> PRIOR APPLICATION NUMBER: US 60/150,604  
28 <151> PRIOR FILING DATE: 1999-08-26  
31 <150> PRIOR APPLICATION NUMBER: US 60/157,108  
32 <151> PRIOR FILING DATE: 1999-10-04  
35 <150> PRIOR APPLICATION NUMBER: US 60/157,756  
36 <151> PRIOR FILING DATE: 1999-10-05  
39 <150> PRIOR APPLICATION NUMBER: US 09/438,046  
40 <151> PRIOR FILING DATE: 1999-11-10  
43 <150> PRIOR APPLICATION NUMBER: US 09/691,200  
44 <151> PRIOR FILING DATE: 2000-10-19  
47 <160> NUMBER OF SEQ ID NOS: 42  
50 <170> SOFTWARE: PatentIn version 3.1  
53 <210> SEQ ID NO: 1  
55 <211> LENGTH: 360  
57 <212> TYPE: DNA  
59 <213> ORGANISM: Homo sapiens  
63 <400> SEQUENCE: 1  
64 aattgtggct gtggaactgt caactggagg tctgcacat gcaattcagg gaaaaccgtg 60  
66 aaaaagtatc atgaggtatt acagtttgag cctggccaca tcaagaggag gggtagagct 120  
68 aagaccatgg ctctagttga catccagttg gatcaccatg aacgatgtga ttgtatctgc 180  
70 agctcaagac cacctcgata agagaatgtg cacatcctta cattaagcct gaaagaacca 240  
72 ttagttttaag gaggggtgaga taagagaccc ttttctacc agcaaccaga cttactacta 300  
74 gcctgcaatg caatgaacac aagtgggtgc tgagtctcag ccttgctttg ttaatgccat 360  
77 <210> SEQ ID NO: 2  
79 <211> LENGTH: 66  
81 <212> TYPE: PRT  
83 <213> ORGANISM: Homo sapiens

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87 &lt;400&gt; SEQUENCE: 2

89 Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser  
 90 1 5 10 15  
 93 Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly  
 94 20 25 30  
 97 His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile  
 98 35 40 45  
 101 Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro  
 102 50 55 60  
 105 Pro Arg  
 106 65

109 &lt;210&gt; SEQ ID NO: 3

111 &lt;211&gt; LENGTH: 690

113 &lt;212&gt; TYPE: DNA

115 &lt;213&gt; ORGANISM: Homo sapiens

119 &lt;400&gt; SEQUENCE: 3

120 ggaagatttc caaccgcag cagcttcaga gaccaactgg aatctgtcac aagctctgtt 60  
 122 tcagggtatc cctataactc tccatcagta acggatccca ctctgattgc ggatgctctg 120  
 124 gacaaaaaaa ttgcagaatt tgatacagtg gaagatctgc tcaagtactt caatccagag 180  
 126 tcatggcaag aagatcttga gaatatgtat ctggacaccc ctcggtatcg aggcagggtca 240  
 128 taccatgacc ggaagtcaaa agttgacctg gataggctca atgatgatgc caagcggtac 300  
 130 agttgcactc ccaggaatta ctcggtcaat ataagagaag agctgaagtt ggccaatgtg 360  
 132 gtcttctttc cacgttgctt cctcgtgcag cgctgtggag gaaattgtgg ctgtggaact 420  
 134 gtcaaactgg agtcctgcac atgcaattca gggaaaaccg tgaaaaagta tcatgaggta 480  
 136 ttacagtttg agcctggcca catcaagagg aggggtagag ctaagaccat ggctctagtt 540  
 138 gacatccagt tggatcacca tgaacgatgc gattgtatct gcagctcaag accacctcga 600  
 140 taagagaatg tgcacatcct tacattaagc ctgaaagaac ctttagttta aggaggggtga 660  
 142 gataagagac ctttttccta ccagcaaccc 690

145 &lt;210&gt; SEQ ID NO: 4

147 &lt;211&gt; LENGTH: 200

149 &lt;212&gt; TYPE: PRT

151 &lt;213&gt; ORGANISM: Homo sapiens

155 &lt;400&gt; SEQUENCE: 4

157 Gly Arg Phe Pro Thr Arg Ser Ser Phe Arg Asp Gln Leu Glu Ser Val  
 158 1 5 10 15  
 161 Thr Ser Ser Val Ser Gly Tyr Pro Tyr Asn Ser Pro Ser Val Thr Asp  
 162 20 25 30  
 165 Pro Thr Leu Ile Ala Asp Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp  
 166 35 40 45  
 169 Thr Val Glu Asp Leu Leu Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu  
 170 50 55 60  
 173 Asp Leu Glu Asn Met Tyr Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser  
 174 65 70 75 80  
 177 Tyr His Asp Arg Lys Ser Lys Val Asp Leu Asp Arg Leu Asn Asp Asp  
 178 85 90 95  
 181 Ala Lys Arg Tyr Ser Cys Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg  
 182 100 105 110  
 185 Glu Glu Leu Lys Leu Ala Asn Val Val Phe Phe Pro Arg Cys Leu Leu  
 186 115 120 125

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189 Val Gln Arg Cys Gly Gly Asn Cys Gly Cys Gly Thr Val Lys Leu Glu
190      130                      135                      140
193 Ser Cys Thr Cys Asn Ser Gly Lys Thr Val Lys Lys Tyr His Glu Val
194 145                      150                      155                      160
197 Leu Gln Phe Glu Pro Gly His Ile Lys Arg Arg Gly Arg Ala Lys Thr
198                      165                      170                      175
201 Met Ala Leu Val Asp Ile Gln Leu Asp His His Glu Arg Cys Asp Cys
202                      180                      185                      190
205 Ile Cys Ser Ser Arg Pro Pro Arg
206      195                      200
209 <210> SEQ ID NO: 5
211 <211> LENGTH: 1934
213 <212> TYPE: DNA
215 <213> ORGANISM: Homo sapiens
219 <220> FEATURE:
221 <221> NAME/KEY: CDS
223 <222> LOCATION: (1)..(966)
225 <223> OTHER INFORMATION:
229 <400> SEQUENCE: 5
230 ttg tac cga aga gat gag acc atc cag gtg aaa gga aac ggc tac gtg      48
231 Leu Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val
232 1                      5                      10                      15
234 cag agt cct aga ttc ccg aac agc tac ccc agg aac ctg ctc ctg aca      96
235 Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr
236      20                      25                      30
238 tgg cgg ctt cac tct cag gag aat aca cgg ata cag cta gtg ttt gac      144
239 Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp
240      35                      40                      45
242 aat cag ttt gga tta gag gaa gca gaa aat gat atc tgt agg tat gat      192
243 Asn Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp
244      50                      55                      60
246 ttt gtg gaa gtt gaa gat ata tcc gaa acc agt acc att att aga gga      240
247 Phe Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly
248 65                      70                      75                      80
250 cga tgg tgt gga cac aag gaa gtt cct cca agg ata aaa tca aga acg      288
251 Arg Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr
252      85                      90                      95
254 aac caa att aaa atc aca ttc aag tcc gat gac tac ttt gtg gct aaa      336
255 Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys
256      100                     105                     110
258 cct gga ttc aag att tat tat tct ttg ctg gaa gat ttc caa ccc gca      384
259 Pro Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala
260      115                     120                     125
262 gca gct tca gag acc aac tgg gaa tct gtc aca agc tct att tca ggg      432
263 Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly
264      130                     135                     140
266 gta tcc tat aac tct cca tca gta acg gat ccc act ctg att gcg gat      480
267 Val Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp
268 145                      150                      155                      160

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270 gct ctg gac aaa aaa att gca gaa ttt gat aca gtg gaa gat ctg ctc      528
271 Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu
272                               165                               170                               175
274 aag tac ttc aat cca gag tca tgg caa gaa gat ctt gag aat atg tat      576
275 Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr
276                               180                               185                               190
278 ctg gac acc cct cgg tat cga ggc agg tca tac cat gac cgg aag tca      624
279 Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser
280                               195                               200                               205
282 aaa gtt gac ctg gat agg ctc aat gat gat gcc aag cgt tac agt tgc      672
283 Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys
284                               210                               215                               220
286 act ccc agg aat tac tcg gtc aat ata aga gaa gag ctg aag ttg gcc      720
287 Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala
288 225                               230                               235                               240
290 aat gtg gtc ttc ttt cca cgt tgc ctc ctc gtg cag cgc tgt gga gga      768
291 Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly
292                               245                               250                               255
294 aat tgt ggc tgt gga act gtc aac tgg agg tcc tgc aca tgc aat tca      816
295 Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser
296                               260                               265                               270
298 ggg aaa acc gtg aaa aag tat cat gag gta tta cag ttt gag cct ggc      864
299 Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly
300                               275                               280                               285
302 cac atc aag agg agg ggt aga gct aag acc atg gct cta gtt gac atc      912
303 His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile
304                               290                               295                               300
306 cag ttg gat cac cat gaa cga tgc gat tgt atc tgc agc tca aga cca      960
307 Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro
308 305                               310                               315                               320
310 cct cga taagagaatg tgcacatcct tacattaagc ctgaaagaac ctttagttta      1016
311 Pro Arg
314 aggagggtga gataagagac ccttttccta ccagcaacca aacttactac tagcctgcaa      1076
316 tgcaatgaac acaagtgggt gctgagtcct agccttgctt tggtaatgcc atggcaagta      1136
318 gaaaggtata tcatcaactt ctatacctaa gaatatagga ttgcatttaa taatagtgtt      1196
320 tgaggttata tatgcacaaa cacacacaga aatatattca tgtctatgtg tatatagatc      1256
322 aaatgttttt tttggtatat ataaccaggt acaccagagc ttacatatgt ttgagttaga      1316
324 ctcttaaaat cctttgccaa aataagggat ggtcaaatat atgaaacatg tctttagaaa      1376
326 atttaggaga taaatttatt tttaaatttt gaaacacaaa acaattttga atcttgctct      1436
328 cttaaagaaa gcattcttga tattaaaaat caaagatga ggctttctta catatacatc      1496
330 ttagttgatt attaaaaaag gaaaaagggt tccagagaaa aggccaatac ctaagcattt      1556
332 tttccatgag aagcactgca tacttaccta tgtggactgt aataacctgt ctccaaaacc      1616
334 atgccataat aatataagtg ctttagaaat taaatcattg tgttttttat gcattttgct      1676
336 gaggcacctt tattcattta acacctatct caaaaactta cttagaagggt tttttattat      1736
338 agtcctacaa aagacaatgt ataagctgta acagaatttt gaattgtttt tctttgcaaa      1796
340 acccctccac aaaagcaaat cctttcaaga atggcatggg cattctgtat gaacctttcc      1856
342 agatgggtgt cagtgaagaa tgtgggtagt tgagaactta aaaagtgaac attgaaacat      1916
344 cgacgtaact ggaaaccg
347 <210> SEQ ID NO: 6

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Input Set : A:\10086623.txt

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349 <211> LENGTH: 322
351 <212> TYPE: PRT
353 <213> ORGANISM: Homo sapiens
357 <400> SEQUENCE: 6
359 Leu Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val
360 1 5 10 15
363 Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr
364 20 25 30
367 Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp
368 35 40 45
371 Asn Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp
372 50 55 60
375 Phe Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly
376 65 70 75 80
379 Arg Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr
380 85 90 95
383 Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys
384 100 105 110
387 Pro Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala
388 115 120 125
391 Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly
392 130 135 140
395 Val Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp
396 145 150 155 160
399 Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu
400 165 170 175
403 Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr
404 180 185 190
407 Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser
408 195 200 205
411 Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys
412 210 215 220
415 Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala
416 225 230 235 240
419 Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly
420 245 250 255
423 Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser
424 260 265 270
427 Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly
428 275 280 285
431 His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile
432 290 295 300
435 Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro
436 305 310 315 320
439 Pro Arg
443 <210> SEQ ID NO: 7
445 <211> LENGTH: 2253
447 <212> TYPE: DNA
449 <213> ORGANISM: Homo sapiens

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→ Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa

## VERIFICATION SUMMARY

DATE: 03/14/2002

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Input Set : A:\10086623.txt

Output Set: N:\CRF3\03142002\J086623.raw

L:19 M:270 C: Current Application Number differs, Replaced Current Application No  
L:19 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:1458 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25  
L:2205 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1  
L:2206 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:42  
L:2206 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1